

SEQUENCE LISTING

<110> Wang, Baiyang

<120> Tissue Factor Antibodies and Uses Thereof

<130> 1861.1670002

<160> 35

<170> PatentIn version 3.2

<210> 1

<211> 915

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(915)

<400> 1

atg gag acc cct gcc tgg ccc cgg gtc ccg cgc ccc gag acc gcc gtc	48
Met Glu Thr Pro Ala Trp Pro Arg Val Pro Arg Pro Glu Thr Ala Val	
1 5 10 15	
gct cgg acg ctc ctg ctc ggc tgg gtc ttc gcc cag gtg gcc ggc gct	96
Ala Arg Thr Leu Leu Leu Gly Trp Val Phe Ala Gln Val Ala Gly Ala	
20 25 30	
tca ggc act aca aat act gtg gca gca tat aat tta act tgg aaa tca	144
Ser Gly Thr Thr Asn Thr Val Ala Ala Tyr Asn Leu Thr Trp Lys Ser	
35 40 45	
act aat ttc aag aca att ttg gag tgg gaa ccc aaa ccc gtc aat caa	192
Thr Asn Phe Lys Thr Ile Leu Glu Trp Glu Pro Lys Pro Val Asn Gln	
50 55 60	
gtc tac act gtt caa ata agc act aag tca gga gat tgg aaa agc aaa	240
Val Tyr Thr Val Gln Ile Ser Thr Lys Ser Gly Asp Trp Lys Ser Lys	
65 70 75 80	
tgc ttt tac aca aca gac aca gag tgt gac ctc acc gac gag att gtg	288
Cys Phe Tyr Thr Thr Asp Thr Glu Cys Asp Leu Thr Asp Glu Ile Val	
85 90 95	
aag gat gtg aag cag acg tac ttg gca cgg gtc ttc tcc tac ccg gca	336
Lys Asp Val Lys Gln Thr Tyr Leu Ala Arg Val Phe Ser Tyr Pro Ala	
100 105 110	
ggg aat gtg gag agc acc ggt tct gct ggg gag cct ctg tat gag aac	384
Gly Asn Val Glu Ser Thr Gly Ser Ala Gly Glu Pro Leu Tyr Glu Asn	
115 120 125	
tcc cca gag ttc aca cct tac ctg gag aca aac ctc gga cag cca aca	432
Ser Pro Glu Phe Thr Pro Tyr Leu Glu Thr Asn Leu Gly Gln Pro Thr	
130 135 140	
att cag agt ttt gaa cag gtg gga aca aaa gtg aat gtg acc gta gaa	480
Ile Gln Ser Phe Glu Gln Val Gly Thr Lys Val Asn Val Thr Val Glu	

145				150				155				160				
gat	gaa	cgg	act	tta	gtc	aga	agg	aac	aac	act	ttc	cta	agc	ctc	cgg	528
Asp	Glu	Arg	Thr	Leu	Val	Arg	Arg	Asn	Asn	Thr	Phe	Leu	Ser	Leu	Arg	
165				170				175								
gat	gtt	ttt	ggc	aag	gac	tta	att	tat	aca	ctt	tat	tat	tgg	aaa	tct	576
Asp	Val	Phe	Gly	Lys	Asp	Leu	Ile	Tyr	Thr	Leu	Tyr	Tyr	Trp	Lys	Ser	
180				185				190								
tca	agt	tca	gga	aag	aaa	aca	gcc	aaa	aca	aac	act	aat	gag	ttt	ttg	624
Ser	Ser	Ser	Gly	Lys	Lys	Thr	Ala	Lys	Thr	Asn	Thr	Asn	Glu	Phe	Leu	
195				200				205								
att	gat	gtg	gat	aaa	gga	gaa	aac	tac	tgt	ttc	agt	gtt	caa	gca	gtg	672
Ile	Asp	Val	Asp	Lys	Gly	Glu	Asn	Tyr	Cys	Phe	Ser	Val	Gln	Ala	Val	
210				215				220								
att	ccc	tcc	cga	aca	gtt	aac	cgg	aag	agt	aca	gac	agc	ccg	gta	gag	720
Ile	Pro	Ser	Arg	Thr	Val	Asn	Arg	Lys	Ser	Thr	Asp	Ser	Pro	Val	Glu	
225				230				235				240				
tgt	atg	ggc	cag	gag	aaa	ggg	gaa	ttc	aga	gaa	ata	ttc	tac	atc	att	768
Cys	Met	Gly	Gln	Glu	Lys	Gly	Glu	Phe	Arg	Glu	Ile	Phe	Tyr	Ile	Ile	
245				250				255								
gga	gct	gtg	gta	ttt	gtg	gtc	atc	atc	ctt	gtc	atc	atc	ctg	gct	ata	816
Gly	Ala	Val	Val	Phe	Val	Val	Ile	Ile	Leu	Val	Ile	Ile	Leu	Ala	Ile	
260				265				270								
tct	cta	cac	aag	tgt	aga	aag	gca	gga	gtg	ggg	cag	agc	tgg	aag	gag	864
Ser	Leu	His	Lys	Cys	Arg	Lys	Ala	Gly	Val	Gly	Gln	Ser	Trp	Lys	Glu	
275				280				285								
aac	tcc	cca	ctg	aat	gtt	tca	aga	gga	tcc	cac	cat	cac	cat	cac	cat	912
Asn	Ser	Pro	Leu	Asn	Val	Ser	Arg	Gly	Ser	His	His	His	His	His	His	
290				295				300								
taa																915

```
<210> 2
<211> 304
<212> PRT
<213> Homo sapiens
```

<400> 2

Met Glu Thr Pro Ala Trp Pro Arg Val Pro Arg Pro Glu Thr Ala Val
1 5 10 15

Ala Arg Thr Leu Leu Leu Gly Trp Val Phe Ala Gln Val Ala Gly Ala
20 25 30

Ser Gly Thr Thr Asn Thr Val Ala Ala Tyr Asn Leu Thr Trp Lys Ser
35 40 45

Thr Asn Phe Lys Thr Ile Leu Glu Trp Glu Pro Lys Pro Val Asn Gln

50		55		60
Val Tyr Thr Val Gln Ile Ser Thr Lys Ser Gly Asp Trp Lys Ser Lys				
65		70		75 80
Cys Phe Tyr Thr Thr Asp Thr Glu Cys Asp Leu Thr Asp Glu Ile Val				
	85		90	95
Lys Asp Val Lys Gln Thr Tyr Leu Ala Arg Val Phe Ser Tyr Pro Ala				
	100		105	110
Gly Asn Val Glu Ser Thr Gly Ser Ala Gly Glu Pro Leu Tyr Glu Asn				
	115		120	125
Ser Pro Glu Phe Thr Pro Tyr Leu Glu Thr Asn Leu Gly Gln Pro Thr				
	130		135	140
Ile Gln Ser Phe Glu Gln Val Gly Thr Lys Val Asn Val Thr Val Glu				
145		150		155 160
Asp Glu Arg Thr Leu Val Arg Arg Asn Asn Thr Phe Leu Ser Leu Arg				
	165		170	175
Asp Val Phe Gly Lys Asp Leu Ile Tyr Thr Leu Tyr Tyr Trp Lys Ser				
	180		185	190
Ser Ser Ser Gly Lys Lys Thr Ala Lys Thr Asn Thr Asn Glu Phe Leu				
	195		200	205
Ile Asp Val Asp Lys Gly Glu Asn Tyr Cys Phe Ser Val Gln Ala Val				
	210		215	220
Ile Pro Ser Arg Thr Val Asn Arg Lys Ser Thr Asp Ser Pro Val Glu				
225		230		235 240
Cys Met Gly Gln Glu Lys Gly Glu Phe Arg Glu Ile Phe Tyr Ile Ile				
	245		250	255
Gly Ala Val Val Phe Val Val Ile Ile Leu Val Ile Ile Leu Ala Ile				
	260		265	270
Ser Leu His Lys Cys Arg Lys Ala Gly Val Gly Gln Ser Trp Lys Glu				
	275		280	285
Asn Ser Pro Leu Asn Val Ser Arg Gly Ser His His His His His				
	290		295	300

<210> 3
 <211> 783
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(783)

<400> 3
 atg gag acc cct gcc tgg ccc cgg gtc ccg cgc ccc gag acc gcc gtc 48
 Met Glu Thr Pro Ala Trp Pro Arg Val Pro Arg Pro Glu Thr Ala Val
 1 5 10 15
 gct cgg acg ctc ctg ctc ggc tgg gtc ttc gcc cag gtg gcc ggc gct 96
 Ala Arg Thr Leu Leu Leu Gly Trp Val Phe Ala Gln Val Ala Gly Ala
 20 25 30
 tca ggc act aca aat act gtg gca gca tat aat tta act tgg aaa tca 144
 Ser Gly Thr Thr Asn Thr Val Ala Tyr Asn Leu Thr Trp Lys Ser
 35 40 45
 act aat ttc aag aca att ttg gag tgg gaa ccc aaa ccc gtc aat caa 192
 Thr Asn Phe Lys Thr Ile Leu Glu Trp Glu Pro Lys Pro Val Asn Gln
 50 55 60
 gtc tac act gtt caa ata agc act aag tca gga gat tgg aaa agc aaa 240
 Val Tyr Thr Val Gln Ile Ser Thr Lys Ser Gly Asp Trp Lys Ser Lys
 65 70 75 80
 tgc ttt tac aca aca gac aca gag tgt gac ctc acc gac gag att gtg 288
 Cys Phe Tyr Thr Thr Asp Thr Glu Cys Asp Leu Thr Asp Glu Ile Val
 85 90 95
 aag gat gtg aag cag acg tac ttg gca cgg gtc ttc tcc tac ccg gca 336
 Lys Asp Val Lys Gln Thr Tyr Leu Ala Arg Val Phe Ser Tyr Pro Ala
 100 105 110
 ggg aat gtg gag agc acc ggt tct gct ggg gag cct ctg tat gag aac 384
 Gly Asn Val Glu Ser Thr Gly Ser Ala Gly Glu Pro Leu Tyr Glu Asn
 115 120 125
 tcc cca gag ttc aca cct tac ctg gag aca aac ctc gga cag cca aca 432
 Ser Pro Glu Phe Thr Pro Tyr Leu Glu Thr Asn Leu Gly Gln Pro Thr
 130 135 140
 att cag agt ttt gaa cag gtg gga aca aaa gtg aat gtg acc gta gaa 480
 Ile Gln Ser Phe Glu Gln Val Gly Thr Lys Val Asn Val Thr Val Glu
 145 150 155 160
 gat gaa cgg act tta gtc aga agg aac aac act ttc cta agc ctc cgg 528
 Asp Glu Arg Thr Leu Val Arg Arg Asn Asn Thr Phe Leu Ser Leu Arg
 165 170 175
 gat gtt ttt ggc aag gac tta att tat aca ctt tat tat tgg aaa tct 576
 Asp Val Phe Gly Lys Asp Leu Ile Tyr Thr Leu Tyr Tyr Trp Lys Ser
 180 185 190

tca agt tca gga aag aaa aca gcc aaa aca aac act aat gag ttt ttg 624
 Ser Ser Ser Gly Lys Lys Thr Ala Lys Thr Asn Thr Asn Glu Phe Leu
 195 200 205

att gat gtg gat aaa gga gaa aac tac tgt ttc agt gtt caa gca gtg 672
 Ile Asp Val Asp Lys Gly Glu Asn Tyr Cys Phe Ser Val Gln Ala Val
 210 215 220

att ccc tcc cga aca gtt aac cgg aag agt aca gac agc ccg gta gag 720
 Ile Pro Ser Arg Thr Val Asn Arg Lys Ser Thr Asp Ser Pro Val Glu
 225 230 235 240

tgt atg ggc cag gag aaa ggg gaa ttc aga gaa aga gga tcc cac cat 768
 Cys Met Gly Gln Glu Lys Gly Glu Phe Arg Glu Arg Gly Ser His His
 245 250 255

cac cat cac cat taa 783
 His His His His
 260

<210> 4
 <211> 260
 <212> PRT
 <213> Homo sapiens

<400> 4

Met Glu Thr Pro Ala Trp Pro Arg Val Pro Arg Pro Glu Thr Ala Val
 1 5 10 15

Ala Arg Thr Leu Leu Leu Gly Trp Val Phe Ala Gln Val Ala Gly Ala
 20 25 30

Ser Gly Thr Thr Asn Thr Val Ala Ala Tyr Asn Leu Thr Trp Lys Ser
 35 40 45

Thr Asn Phe Lys Thr Ile Leu Glu Trp Glu Pro Lys Pro Val Asn Gln
 50 55 60

Val Tyr Thr Val Gln Ile Ser Thr Lys Ser Gly Asp Trp Lys Ser Lys
 65 70 75 80

Cys Phe Tyr Thr Thr Asp Thr Glu Cys Asp Leu Thr Asp Glu Ile Val
 85 90 95

Lys Asp Val Lys Gln Thr Tyr Leu Ala Arg Val Phe Ser Tyr Pro Ala
 100 105 110

Gly Asn Val Glu Ser Thr Gly Ser Ala Gly Glu Pro Leu Tyr Glu Asn
 115 120 125

Ser Pro Glu Phe Thr Pro Tyr Leu Glu Thr Asn Leu Gly Gln Pro Thr

130		135		140
Ile Gln Ser Phe Glu Gln Val Gly Thr Lys Val Asn Val Thr Val Glu				
145		150		155 160
Asp Glu Arg Thr Leu Val Arg Arg Asn Asn Thr Phe Leu Ser Leu Arg				
	165		170	175
Asp Val Phe Gly Lys Asp Leu Ile Tyr Thr Leu Tyr Tyr Trp Lys Ser				
	180		185	190
Ser Ser Ser Gly Lys Lys Thr Ala Lys Thr Asn Thr Asn Glu Phe Leu				
	195		200	205
Ile Asp Val Asp Lys Gly Glu Asn Tyr Cys Phe Ser Val Gln Ala Val				
	210		215	220
Ile Pro Ser Arg Thr Val Asn Arg Lys Ser Thr Asp Ser Pro Val Glu				
	225		230	235 240
Cys Met Gly Gln Glu Lys Gly Glu Phe Arg Glu Arg Gly Ser His His				
	245		250	255
His His His His				
	260			

<210> 5
 <211> 350
 <212> DNA
 <213> Mus sp.

<220>
 <221> CDS
 <222> (1) .. (348)

<400> 5	
cag gtg cag ctg aag cag tct gga gct gag ctg atg aag cct ggg gcc	48
Gln Val Gln Leu Lys Gln Ser Gly Ala Glu Leu Met Lys Pro Gly Ala	
1 5 10 15	
tca gtg aag ata tcc tgc aag gct act ggc tac aca ttc agt agc tac	96
Ser Val Lys Ile Ser Cys Lys Ala Thr Gly Tyr Thr Phe Ser Ser Tyr	
20 25 30	
tgg ata gag tgg gta aag cag agg cct gga cat ggc ctt gag tgg att	144
Trp Ile Glu Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp Ile	
35 40 45	
gga gag att tta cct gga agt ggt agt act aac tac aat gag aag ttc	192
Gly Glu Ile Leu Pro Gly Ser Gly Ser Thr Asn Tyr Asn Glu Lys Phe	
50 55 60	

aag ggc aag gcc aca ttc act gca gat aca tcc tcc aac aca gcc tac 240
Lys Gly Lys Ala Thr Phe Thr Ala Asp Thr Ser Ser Asn Thr Ala Tyr
65 70 75 80

atg caa ctc agc agc ctg aca tct gag gac tct gcc gtc tat tac tgt 288
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

gca aga gag gat agg tac gac ggt gac tac tgg ggc caa ggc acc act 336
Ala Arg Glu Asp Arg Tyr Asp Gly Asp Tyr Trp Gly Gln Gly Thr Thr
100 105 110

ctc aca gtc tcg ag 350
Leu Thr Val Ser
115

<210> 6
<211> 116
<212> PRT
<213> Mus sp.

<400> 6

Gln Val Gln Leu Lys Gln Ser Gly Ala Glu Leu Met Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Ile Ser Cys Lys Ala Thr Gly Tyr Thr Phe Ser Ser Tyr
20 25 30

Trp Ile Glu Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp Ile
35 40 45

Gly Glu Ile Leu Pro Gly Ser Gly Ser Thr Asn Tyr Asn Glu Lys Phe
50 55 60

Lys Gly Lys Ala Thr Phe Thr Ala Asp Thr Ser Ser Asn Thr Ala Tyr
65 70 75 80

Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Asp Arg Tyr Asp Gly Asp Tyr Trp Gly Gln Gly Thr Thr
100 105 110

Leu Thr Val Ser
115

<210> 7
<211> 337
<212> DNA
<213> Mus sp.

<220>

<221> CDS

<222> (1) .. (336)

<400> 7

cag	gct	ggt	gtg	act	cag	gaa	tct	gca	ctc	acc	aca	tca	cct	ggt	gaa	48
Gln	Ala	Val	Val	Thr	Gln	Glu	Ser	Ala	Leu	Thr	Thr	Ser	Pro	Gly	Glu	
1				5					10					15		

aca	gtc	aca	ctc	act	tgt	cgc	tca	agt	act	ggg	gct	ggt	aca	act	agt	96
Thr	Val	Thr	Leu	Thr	Cys	Arg	Ser	Ser	Thr	Gly	Ala	Val	Thr	Thr	Ser	
			20					25					30			

aac	tat	gcc	aac	tgg	gtc	caa	gaa	aaa	cca	gat	cat	tta	ttc	act	ggt	144
Asn	Tyr	Ala	Asn	Trp	Val	Gln	Glu	Lys	Pro	Asp	His	Leu	Phe	Thr	Gly	
		35					40					45				

cta	ata	ggt	ggt	acc	aac	aac	cga	gct	cca	ggt	ggt	cct	gcc	aga	ttc	192
Leu	Ile	Gly	Gly	Thr	Asn	Asn	Arg	Ala	Pro	Gly	Val	Pro	Ala	Arg	Phe	
	50					55				60						

tca	ggc	tcc	ctg	att	gga	gac	aag	gct	gcc	ctc	acc	atc	aca	ggg	gca	240
Ser	Gly	Ser	Leu	Ile	Gly	Asp	Lys	Ala	Ala	Leu	Thr	Ile	Thr	Gly	Ala	
65					70					75				80		

cag	act	gag	gat	gag	gca	ata	tat	ttc	tgt	gct	cta	tgg	tac	agc	aac	288
Gln	Thr	Glu	Asp	Glu	Ala	Ile	Tyr	Phe	Cys	Ala	Leu	Trp	Tyr	Ser	Asn	
				85					90					95		

cac	tgg	gtg	ttc	ggt	gga	gga	acc	aaa	ctg	act	gtc	cta	ggt	cag	ccc	c	337
His	Trp	Val	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Thr	Val	Leu	Gly	Gln	Pro		
			100					105					110				

<210> 8

<211> 112

<212> PRT

<213> Mus sp.

<400> 8

Gln	Ala	Val	Val	Thr	Gln	Glu	Ser	Ala	Leu	Thr	Thr	Ser	Pro	Gly	Glu
1				5					10					15	

Thr	Val	Thr	Leu	Thr	Cys	Arg	Ser	Ser	Thr	Gly	Ala	Val	Thr	Thr	Ser
			20					25					30		

Asn	Tyr	Ala	Asn	Trp	Val	Gln	Glu	Lys	Pro	Asp	His	Leu	Phe	Thr	Gly
		35					40					45			

Leu	Ile	Gly	Gly	Thr	Asn	Asn	Arg	Ala	Pro	Gly	Val	Pro	Ala	Arg	Phe
	50					55				60					

Ser	Gly	Ser	Leu	Ile	Gly	Asp	Lys	Ala	Ala	Leu	Thr	Ile	Thr	Gly	Ala
65					70					75				80	

Gln Thr Glu Asp Glu Ala Ile Tyr Phe Cys Ala Leu Trp Tyr Ser Asn
85 90 95

His Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln Pro
100 105 110

<210> 9
<211> 351
<212> DNA
<213> Mus sp.

<220>
<221> CDS
<222> (1)..(351)

<400> 9
cag gtg cag ctg aag cag tct gga cct gag ctg gag aag cct ggc gct 48
Gln Val Gln Leu Lys Gln Ser Gly Pro Glu Leu Glu Lys Pro Gly Ala
1 5 10 15
tca gtg aag ata tcc tgc aag gct tct ggt tac tca ttc act ggc tac 96
Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Gly Tyr
20 25 30
aac atg aac tgg gtg aag cag agc aat gga aag agc ctt gag tgg att 144
Asn Met Asn Trp Val Lys Gln Ser Asn Gly Lys Ser Leu Glu Trp Ile
35 40 45
gga aat att gat cct tac tat ggt ggt act agc tac aac cag aag ttc 192
Gly Asn Ile Asp Pro Tyr Tyr Gly Gly Thr Ser Tyr Asn Gln Lys Phe
50 55 60
aag ggc aag gcc aca ttg act gta gac aaa tcc tcc aac aca gcc tac 240
Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Asn Thr Ala Tyr
65 70 75 80
atg cac ctc aag agc ctg aca tct gag gac tct gca gtc tat tac tgt 288
Met His Leu Lys Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95
gca aga gat agt agc tcc tgg ttt gct tac tgg ggc caa ggg act ctg 336
Ala Arg Asp Ser Ser Ser Trp Phe Ala Tyr Trp Gly Gln Gly Thr Leu
100 105 110
gtc act gtc tct gca 351
Val Thr Val Ser Ala
115

<210> 10
<211> 117
<212> PRT
<213> Mus sp.

<400> 10

Gln Val Gln Leu Lys Gln Ser Gly Pro Glu Leu Glu Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Gly Tyr
20 25 30

Asn Met Asn Trp Val Lys Gln Ser Asn Gly Lys Ser Leu Glu Trp Ile
35 40 45

Gly Asn Ile Asp Pro Tyr Tyr Gly Gly Thr Ser Tyr Asn Gln Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Asn Thr Ala Tyr
65 70 75 80

Met His Leu Lys Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Ser Ser Ser Trp Phe Ala Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ala
115

<210> 11
<211> 325
<212> DNA
<213> Mus sp.

<220>
<221> CDS
<222> (1)..(324)

<400> 11
gac atc cag ctg act cag tct cca gcc tcc cta tct gca tct gtg gga 48
Asp Ile Gln Leu Thr Gln Ser Pro Ala Ser Leu Ser Ala Ser Val Gly
1 5 10 15
gaa act gtc acc atc aca tgt cga gca agt ggg aat att cac aat tat 96
Glu Thr Val Thr Ile Thr Cys Arg Ala Ser Gly Asn Ile His Asn Tyr
20 25 30
tta gca tgg tat cag cag aaa cag gga aaa tct cct cag ctc ctg gtc 144
Leu Ala Trp Tyr Gln Gln Lys Gln Gly Lys Ser Pro Gln Leu Leu Val
35 40 45
tat aat gca aaa acc tta gca gat ggt gtg cca tca agg ttc agt ggc 192
Tyr Asn Ala Lys Thr Leu Ala Asp Gly Val Pro Ser Arg Phe Ser Gly
50 55 60
agt gga tca gga aca caa tat tct ctc aag atc aac agc ctg cag cct 240
Ser Gly Ser Gly Thr Gln Tyr Ser Leu Lys Ile Asn Ser Leu Gln Pro

65					70					75					80					
gaa	gat	ttt	ggg	agt	tat	tac	tgt	caa	cat	ttt	tgg	att	act	ccg	tgg	288				
Glu	Asp	Phe	Gly	Ser	Tyr	Tyr	Cys	Gln	His	Phe	Trp	Ile	Thr	Pro	Trp					
					85					90					95					

acg ttc ggt gga ggc acc aag ctg gag atc taa cgg a 325
Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Arg
100 105

<210>	12
<211>	106
<212>	PRT
<213>	Mus sp.

<400> 12

Asp Ile Gln Leu Thr Gln Ser Pro Ala Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Glu Thr Val Thr Ile Thr Cys Arg Ala Ser Gly Asn Ile His Asn Tyr
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Gln Gly Lys Ser Pro Gln Leu Leu Val
35 40 45

Tyr Asn Ala Lys Thr Leu Ala Asp Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Gln Tyr Ser Leu Lys Ile Asn Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Gly Ser Tyr Tyr Cys Gln His Phe Trp Ile Thr Pro Trp
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
100 105

<210>	13
<211>	20
<212>	DNA
<213>	Unknown

<220>
<223> PCR primer TF4

```
<400> 13
acggaacccg ctcgatctcg                                     20
```

$\langle 210 \rangle$	14
$\langle 211 \rangle$	20
$\langle 212 \rangle$	DNA

<213> Unknown

<220>
<223> PCR primer TF5

<400> 14
cgtgacaacc tcgatgacgt 20

<210> 15
<211> 35
<212> DNA
<213> Unknown

<220>
<223> PCR primer TF1

<400> 15
atctgcggat ccaccatgga gaccctgcc tggcc 35

<210> 16
<211> 66
<212> DNA
<213> Unknown

<220>
<223> PCR primer TF3

<400> 16
atctgcctcg agttaatggt gatggtgatg gtgggaccc ctttctctga attccccttt 60
ctcctg 66

<210> 17
<211> 66
<212> DNA
<213> Unknown

<220>
<223> PCR primer TF1

<400> 17
atctgcctcg agttaatggt gatggtgatg gtgggaccc cttgaaacat tcagtgggga 60
gttctc 66

<210> 18
<211> 363
<212> DNA
<213> Mus sp.

<220>
<221> CDS
<222> (1) .. (363)

<400> 18
gag gtc cag ctg cag caa tct gga gct gag ctg atg aag cct ggg gcc 48

Glu	Val	Gln	Leu	Gln	Gln	Ser	Gly	Ala	Glu	Leu	Met	Lys	Pro	Gly	Ala		
1				5					10					15			
tca	gtg	aag	ata	tcc	tgc	aag	gct	act	ggc	tac	aca	ttc	agt	agc	tac		96
Ser	Val	Lys	Ile	Ser	Cys	Lys	Ala	Thr	Gly	Tyr	Thr	Phe	Ser	Ser	Tyr		
			20					25					30				
tgg	ata	gag	tgg	gta	aag	cag	agg	cct	gga	cat	ggc	ctt	gag	tgg	att		144
Trp	Ile	Glu	Trp	Val	Lys	Gln	Arg	Pro	Gly	His	Gly	Leu	Glu	Trp	Ile		
		35					40					45					
gga	gag	att	tta	cct	gga	agt	gct	agt	act	aag	tac	aat	gag	aag	ttc		192
Gly	Glu	Ile	Leu	Pro	Gly	Ser	Ala	Ser	Thr	Lys	Tyr	Asn	Glu	Lys	Phe		
	50					55					60						
aag	ggc	aag	gcc	aca	ttc	act	gca	gat	aca	tcc	tcc	aac	aca	gcc	tac		240
Lys	Gly	Lys	Ala	Thr	Phe	Thr	Ala	Asp	Thr	Ser	Ser	Asn	Thr	Ala	Tyr		
	65				70				75						80		
atg	caa	ctc	agc	agc	ctg	aca	tct	gag	gac	tct	gcc	gtc	tat	tac	tgt		288
Met	Gln	Leu	Ser	Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Val	Tyr	Tyr	Cys		
				85					90					95			
gca	agag	gat	tat	tac	tac	ggt	agt	agc	tac	ggg	ttt	gct	tac	tgg	ggc		336
Ala	Arg	Asp	Tyr	Tyr	Tyr	Gly	Ser	Ser	Tyr	Gly	Phe	Ala	Tyr	Trp	Gly		
			100					105					110				
caa	ggg	act	ctg	gtc	act	gtc	tcg	agt									363
Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser									
			115				120										

<210> 19
 <211> 121
 <212> PRT
 <213> Mus sp.

<400> 19

Glu	Val	Gln	Leu	Gln	Gln	Ser	Gly	Ala	Glu	Leu	Met	Lys	Pro	Gly	Ala		
1				5					10					15			
Ser	Val	Lys	Ile	Ser	Cys	Lys	Ala	Thr	Gly	Tyr	Thr	Phe	Ser	Ser	Tyr		
			20					25					30				
Trp	Ile	Glu	Trp	Val	Lys	Gln	Arg	Pro	Gly	His	Gly	Leu	Glu	Trp	Ile		
		35					40					45					
Gly	Glu	Ile	Leu	Pro	Gly	Ser	Ala	Ser	Thr	Lys	Tyr	Asn	Glu	Lys	Phe		
	50					55					60						
Lys	Gly	Lys	Ala	Thr	Phe	Thr	Ala	Asp	Thr	Ser	Ser	Asn	Thr	Ala	Tyr		
	65				70				75						80		
Met	Gln	Leu	Ser	Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Val	Tyr	Tyr	Cys		
				85					90					95			

Ala Arg Asp Tyr Tyr Tyr Gly Ser Ser Tyr Gly Phe Ala Tyr Trp Gly
 100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 20
 <211> 330
 <212> DNA
 <213> Mus sp.

<220>
 <221> CDS
 <222> (1)..(330)

<400> 20
 cag gct gtt gtg act cag gaa tct gca ctc acc aca tca cct ggt gaa 48
 Gln Ala Val Val Thr Gln Glu Ser Ala Leu Thr Thr Ser Pro Gly Glu
 1 5 10 15
 aca gtc aca ctc act tgt cgc tca agt act ggg gct gtt aca act agt 96
 Thr Val Thr Leu Thr Cys Arg Ser Ser Thr Gly Ala Val Thr Thr Ser
 20 25 30
 aac tat gcc aac tgg gtc caa gaa aaa cca gat cat tta ttc act ggc 144
 Asn Tyr Ala Asn Trp Val Gln Glu Lys Pro Asp His Leu Phe Thr Gly
 35 40 45
 cta ata ggt ggt acc aac aac cga ggt cca ggt gtt cct gcc aga ttc 192
 Leu Ile Gly Gly Thr Asn Asn Arg Gly Pro Gly Val Pro Ala Arg Phe
 50 55 60
 tca ggc tcc ctg att gga gac aag gct gcc ctc acc atc aca ggg gca 240
 Ser Gly Ser Leu Ile Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
 65 70 75 80
 cag act gag gat gag gca gta tat ttc tgt gct cta tgg tac agc aac 288
 Gln Thr Glu Asp Glu Ala Val Tyr Phe Cys Ala Leu Trp Tyr Ser Asn
 85 90 95
 cat tgg gtg ttc ggt gga gga acc aaa ctg act gtc cta ggt 330
 His Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
 100 105 110

<210> 21
 <211> 110
 <212> PRT
 <213> Mus sp.

<400> 21

Gln Ala Val Val Thr Gln Glu Ser Ala Leu Thr Thr Ser Pro Gly Glu
 1 5 10 15

Thr Val Thr Leu Thr Cys Arg Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Glu Lys Pro Asp His Leu Phe Thr Gly
35 40 45

Leu Ile Gly Gly Thr Asn Asn Arg Gly Pro Gly Val Pro Ala Arg Phe
50 55 60

Ser Gly Ser Leu Ile Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Thr Glu Asp Glu Ala Val Tyr Phe Cys Ala Leu Trp Tyr Ser Asn
85 90 95

His Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
100 105 110

<210> 22
<211> 354
<212> DNA
<213> Mus sp.

<220>
<221> CDS
<222> (1) .. (354)

<400> 22
cag gtc caa ctg cag cag cct ggg gct gag ctt gtg aag cct ggg gct 48
Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Lys Pro Gly Ala
1 5 10 15
tca gtg aag ctg tcc tgc aag act tct ggc tac acc ttc acc agc tac 96
Ser Val Lys Leu Ser Cys Lys Thr Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30
tgg atg cac tgg gtg aag cag agg cct gga caa ggc ctt gag tgg atc 144
Trp Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45
gga gag att gat cct tct gat agt tat act aac tac aat caa aag ttc 192
Gly Glu Ile Asp Pro Ser Asp Ser Tyr Thr Asn Tyr Asn Gln Lys Phe
50 55 60
aag ggc aag gcc aca ttg act gta gac aaa tcc tcc agc aca gcc tac 240
Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80
atg cag ctc agc agc ctg aca tct gag gac tct gcg gtc tat tac tgt 288
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95
acc tac tat gtt aac tac tat gct atg gac tac tgg ggt caa gga acc 336
Thr Tyr Tyr Val Asn Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr

100 105 110 354
tca gtc acc gtc tcc tca
Ser Val Thr Val Ser Ser
115

<210> 23
<211> 118
<212> PRT
<213> Mus sp.

<400> 23

Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Leu Ser Cys Lys Thr Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Trp Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Glu Ile Asp Pro Ser Asp Ser Tyr Thr Asn Tyr Asn Gln Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Thr Tyr Tyr Val Asn Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Ser Val Thr Val Ser Ser
115

<210> 24
<211> 318
<212> DNA
<213> Mus sp.

<220>
<221> CDS
<222> (1)..(318)

<400> 24

caa att gtt ctc acc cag tct cca gca atc atg tct gca tct cta ggg 48
Gln Ile Val Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Leu Gly
1 5 10 15

gag gag atc acc cta acc tgc agt gcc agc tcg agt gta agt tac atg 96
Glu Glu Ile Thr Leu Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met
20 25 30

cac tgg tac cag cag aag tca ggc act tct ccc aaa ctc ttg att tat 144
His Trp Tyr Gln Gln Lys Ser Gly Thr Ser Pro Lys Leu Leu Ile Tyr
35 40 45

agc aca tcc aac ctg gct tct gga gtc cct tct cgc ttc agt ggc agt 192
Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
50 55 60

ggg tct ggg acc ttt tat tct ctc aca atc agc agt gtg gag gct gaa 240
Gly Ser Gly Thr Phe Tyr Ser Leu Thr Ile Ser Ser Val Glu Ala Glu
65 70 75 80

gat gct gcc gat tat tac tgc cat cag tgg agt agt tat cca tac acg 288
Asp Ala Ala Asp Tyr Tyr Cys His Gln Trp Ser Ser Tyr Pro Tyr Thr
85 90 95

ttc gga ggg ggg acc aag ctg gaa ata aaa 318
Phe Gly Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 25
<211> 106
<212> PRT
<213> Mus sp.

<400> 25

Gln Ile Val Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Leu Gly
1 5 10 15

Glu Glu Ile Thr Leu Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met
20 25 30

His Trp Tyr Gln Gln Lys Ser Gly Thr Ser Pro Lys Leu Leu Ile Tyr
35 40 45

Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Phe Tyr Ser Leu Thr Ile Ser Ser Val Glu Ala Glu
65 70 75 80

Asp Ala Ala Asp Tyr Tyr Cys His Gln Trp Ser Ser Tyr Pro Tyr Thr
85 90 95

Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 26

<211> 360
<212> DNA
<213> Mus sp.

<220>
<221> CDS
<222> (1)..(360)

<400> 26
cag gtg cag ctg aag gag tct gga gct gag ctg atg aag cct ggg gcc 48
Gln Val Gln Leu Lys Glu Ser Gly Ala Glu Leu Met Lys Pro Gly Ala
1 5 10 15

tca gtg aag ata tcc tgc aag gct act ggc tac aca ttc agt agc tac 96
Ser Val Lys Ile Ser Cys Lys Ala Thr Gly Tyr Thr Phe Ser Ser Tyr
20 25 30

tgg ata gag tgg gta aag cag agg cct gga cat ggc ctt gag tgg att 144
Trp Ile Glu Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp Ile
35 40 45

gga gag att tta cct gga agt ggt agt act aac tac aat gag aag ttc 192
Gly Glu Ile Leu Pro Gly Ser Gly Ser Thr Asn Tyr Asn Glu Lys Phe
50 55 60

aag ggc aag gcc aca ttc act gca gat aca tcc tcc aac aca gcc tac 240
Lys Gly Lys Ala Thr Phe Thr Ala Asp Thr Ser Ser Asn Thr Ala Tyr
65 70 75 80

atg caa ctc agc agc ctg aca tct gag gac tct gcc gtc tat tac tgt 288
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

gca aga gac agg aac ggc tac gtg aac tac ttt gac tcc tgg ggc caa 336
Ala Arg Asp Arg Asn Gly Tyr Val Asn Tyr Phe Asp Ser Trp Gly Gln
100 105 110

ggc acc act ctc aca gtc tcc tca 360
Gly Thr Thr Leu Thr Val Ser Ser
115 120

<210> 27
<211> 120
<212> PRT
<213> Mus sp.

<400> 27
Gln Val Gln Leu Lys Glu Ser Gly Ala Glu Leu Met Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Ile Ser Cys Lys Ala Thr Gly Tyr Thr Phe Ser Ser Tyr
20 25 30

Trp Ile Glu Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp Ile
35 40 45

Gly Glu Ile Leu Pro Gly Ser Gly Ser Thr Asn Tyr Asn Glu Lys Phe
50 55 60

Lys Gly Lys Ala Thr Phe Thr Ala Asp Thr Ser Ser Asn Thr Ala Tyr
65 70 75 80

Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Arg Asn Gly Tyr Val Asn Tyr Phe Asp Ser Trp Gly Gln
100 105 110

Gly Thr Thr Leu Thr Val Ser Ser
115 120

<210> 28
<211> 351
<212> DNA
<213> Mus sp.

<220>
<221> CDS
<222> (1) .. (351)

<400> 28
gat gtg aag ctt cag gag tca gga cct gac ctg gtg aaa cct tct cag 48
Asp Val Lys Leu Gln Glu Ser Gly Pro Asp Leu Val Lys Pro Ser Gln
1 5 10 15

tca ctt tca ctc acc tgc act gtc act ggc tac tcc atc acc agt ggt 96
Ser Leu Ser Leu Thr Cys Thr Val Thr Gly Tyr Ser Ile Thr Ser Gly
20 25 30

tat agc tgg cac tgg atc cgg cag ttt cca gga aac aaa ctg gaa tgg 144
Tyr Ser Trp His Trp Ile Arg Gln Phe Pro Gly Asn Lys Leu Glu Trp
35 40 45

atg ggc tac ata cac tac agt ggt agc act aag tac aac cca tct ctc 192
Met Gly Tyr Ile His Tyr Ser Gly Ser Thr Lys Tyr Asn Pro Ser Leu
50 55 60

aaa agt cga atc tct atc act cga gac aca tcc aag aac cag ttc ttc 240
Lys Ser Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn Gln Phe Phe
65 70 75 80

ctg cag ttg aat tct gtg act act gag gac aca gcc aca tat tac tgt 288
Leu Gln Leu Asn Ser Val Thr Thr Glu Asp Thr Ala Thr Tyr Tyr Cys
85 90 95

gca aga ctc tgg agt tgg tac ttc gat gtc tgg ggc gca ggg acc acg 336
Ala Arg Leu Trp Ser Trp Tyr Phe Asp Val Trp Gly Ala Gly Thr Thr
100 105 110

gtc acc gtc tcc tca 351

Val Thr Val Ser Ser
115

<210> 29
<211> 117
<212> PRT
<213> Mus sp.

<400> 29

Asp Val Lys Leu Gln Glu Ser Gly Pro Asp Leu Val Lys Pro Ser Gln
1 5 10 15

Ser Leu Ser Leu Thr Cys Thr Val Thr Gly Tyr Ser Ile Thr Ser Gly
20 25 30

Tyr Ser Trp His Trp Ile Arg Gln Phe Pro Gly Asn Lys Leu Glu Trp
35 40 45

Met Gly Tyr Ile His Tyr Ser Gly Ser Thr Lys Tyr Asn Pro Ser Leu
50 55 60

Lys Ser Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn Gln Phe Phe
65 70 75 80

Leu Gln Leu Asn Ser Val Thr Thr Glu Asp Thr Ala Thr Tyr Tyr Cys
85 90 95

Ala Arg Leu Trp Ser Trp Tyr Phe Asp Val Trp Gly Ala Gly Thr Thr
100 105 110

Val Thr Val Ser Ser
115

<210> 30
<211> 336
<212> DNA
<213> Mus sp.

<220>
<221> CDS
<222> (1)..(336)

<400> 30

aac att atg atg aca cag tcg cca tca tct ctg gct gtg tct gca gga 48
Asn Ile Met Met Thr Gln Ser Pro Ser Ser Leu Ala Val Ser Ala Gly
1 5 10 15

gaa aag gtc act atg agc tgt aag tcc agt caa agt gtt tta tac agt 96
Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
20 25 30

tca aat cag aag aac tac ttg gcc tgg tac cag cag aaa cca ggg cag 144
Ser Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

tct cct aaa ctg ctg atc tac tgg gca tcc act agg gaa tct ggt gtc 192
Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

cct gat cgc ttc aca ggc agt gga tct ggg aca gat ttt act ctt acc 240
Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

atc agc agt gta caa gct gaa gac ctg gca gtt tat tac tgt cat caa 288
Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr Tyr Cys His Gln
85 90 95

tac ctc tcc tcg tac acg ttc gga ggg ggg acc aag ctg gaa ata aaa 336
Tyr Leu Ser Ser Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 31
<211> 112
<212> PRT
<213> Mus sp.

<400> 31

Asn Ile Met Met Thr Gln Ser Pro Ser Ser Leu Ala Val Ser Ala Gly
1 5 10 15

Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
20 25 30

Ser Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr Tyr Cys His Gln
85 90 95

Tyr Leu Ser Ser Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 32
<211> 57
<212> DNA
<213> Unknown

<220>
<223> Signal sequence peptide

<220>
<221> CDS
<222> (1)..(57)

<400> 32
atg gct tgg gtg tgg acc ttg cta ttc ctg atg gca gct gcc caa agt 48
Met Ala Trp Val Trp Thr Leu Leu Phe Leu Met Ala Ala Ala Gln Ser
1 5 10 15

gcc caa gca 57
Ala Gln Ala

<210> 33
<211> 19
<212> PRT
<213> Unknown

<220>
<223> Synthetic Construct

<400> 33

Met Ala Trp Val Trp Thr Leu Leu Phe Leu Met Ala Ala Ala Gln Ser
1 5 10 15

Ala Gln Ala

<210> 34
<211> 60
<212> DNA
<213> Unknown

<220>
<223> Signal sequence peptide

<220>
<221> CDS
<222> (1)..(60)

<400> 34
atg gaa tca cag act cag gtc ttc ctc tcc ctg ctg ctc tgg ata tct 48
Met Glu Ser Gln Thr Gln Val Phe Leu Ser Leu Leu Leu Trp Ile Ser
1 5 10 15

ggt acc tgt ggg 60
Gly Thr Cys Gly
20

<210> 35
<211> 20

<212> PRT
<213> Unknown

<220>
<223> Synthetic Construct

<400> 35

Met	Glu	Ser	Gln	Thr	Gln	Val	Phe	Leu	Ser	Leu	Leu	Leu	Trp	Ile	Ser
1				5					10					15	

Gly	Thr	Cys	Gly
			20